

KLAIPĖDOS UNIVERSITETAS

13th EUROPEAN CONGRESS
OF ICHTHYOLOGY

6th – 12th September

Klaipėda, Lithuania

Abstract book

Klaipėda, 2009

Genetic characterization of common carp (*Cyprinus carpio* L.) populations from Greece using mitochondrial DNA sequences

Anastasia Imsiridou¹, Alexandros Triantafyllidis², Athanasios D. Baxevanis² & Costas Triantaphyllidis²

¹Department of Fisheries and Aquaculture Technology, Alexander Technological Educational Institute of Thessaloniki, P.O. Box 157, GR-63200 Nea Moudania, Halkidiki, Greece; e-mail: imsi@otenet.gr

²Department of Genetics, Development and Molecular Biology, Aristotle University, School of Biology, GR-54124 Thessaloniki, Macedonia, Greece

Introduction

Common carp (*Cyprinus carpio* L., 1758) is divided generally into two subspecies, *Cyprinus carpio carpio* from Europe and *Cyprinus carpio haematopterus* from Asia. The species is considered to be native to Greece. However, during the late 1980s and the 1990s many introductions with fry or fingerlings belonging to the Central European race (Hungary) were made into many natural lakes of Greece (e.g. Koroncia, Volvi) as well as into Greek rivers (e.g. Evros, Aliakmonas). The aim of this study was the genetic characterization of common carp from two lakes (Volvi, Doirani) and two rivers (Evros, Aliakmonas) in Greece as well as the study of the phylogenetic relationships of common carp from Greece with European and East Asian groups.

Materials and methods

Fourteen individuals of wild common carp were analyzed. PCR was applied to amplify a segment of control region and the complete sequence of cytochrome b gene of mitochondrial DNA. A sequencing analysis was followed and DNA sequences were deposited in GenBank (accession numbers EU 689059 – EU 689086). Phylogenetic reconstruction was implemented using MEGA v3.1 program and PAUP* 4.0b10. Similar sequences of one individual from Yangtze River (China- South East Asia) and of one individual from Volga River (Russia - Europe), were used for the phylogenetic analysis. *Carassius auratus langsdorffii* was used as outgroup.

Results

In total 646 bp at the 5' end of the mtDNA control region, as well as 1119 bp for the cyt b were sequenced. A total of 9 variable singleton sites and 7 unique haplotypes were found. A common haplotype was shared among one individual from Lake Volvi (H1), two individuals from Lake Doirani and among all three individuals from Evros River. This haplotype was the same also in the sample from Volga River. Neighbour – Joining dendrogram revealed that all Greek haplotypes were clustered together with the Volga River haplotype (H1) in the same group, whereas the haplotype from Yangtze River seems to be the most genetically distinct in a separate branch.

Discussion

In two out of the four populations studied, only one haplotype was found. Similar loss of sequence variation was reported for European common carp which suggests a history of founder effects and small effective population size. The five different haplotypes found in Lake Volvi, could represent different common carp stocks, after many introductions and translocations that have been made repeatedly in this lake. The H1 haplotype could be the ancestral one, which represents the European origin of common carp populations from Greece or could be justified by the introductions reported with fry or fingerlings belonging to the Central European race, into many natural habitats in Greece. The phylogenetic analysis reveals that populations of common carp from Greece belong to the European group of populations and to the subspecies *C. c. carpio*.

Karyotypes of the Sakhalin sturgeon *Acipenser mikadoi* and the Amur sturgeon *A. schrenckii*: how many polyploid events took place in Acipenserid evolution?

Victor Vasil'ev¹, Ekaterina Vasil'eva², Sergei Shedko³ and German Novomodny⁴

¹Institute of Ecology and Evolution, RAS;

²Zoological Museum of the Moscow State University, e-mail: vas_katerina@mail.ru;

³Institute of Biology and Soil Sciences, Far East Branch of Russian Academy of Sciences;

⁴Khabarovsk branch of FGUP TINRO-Center

Zoogeography and Evolution

The karyotypes of the Sakhalin sturgeon *Acipenser mikadoi* and the Amur sturgeon *A. schrenckii* were investigated. The karyotype of *A. mikadoi* includes 262±4 chromosomes; the number of banded chromosome is 80, and the number of chromosome arms 342±4. The karyotype of *A. schrenckii* includes 266±4 chromosomes; the number of banded chromosome is 92, and the number of chromosome arms 358±4. The obtained results prove the Sakhalin sturgeon to be octoploid species for the first time and reject its previous classification as 16-ploid species with about 500 chromosomes conducted from the nuclear DNA content study (Birstein et al. 1993). The comparative analysis of cytogenetic

and morphological data demonstrates the validity of this species which differs from the North American green sturgeon *A. medirostris* in the karyotype structure, the nuclear DNA content value, and several morphological characters.

Ludwig et al. (2001) suppose four polyploidization events in Acipenserid phylogeny: the first one occurred in the ancestor of polyploid Atlantic species, the second one occurred in the ancestor of *A. schrenckii* - *A. transmontanus* - *A. sinensis* subclade, the third one occurred in the phylum including *A. mikadoi* and *A. medirostris*, and the fourth one resulted in the origin of *A. mikadoi*. Birstein (2005) recognizes seven polyploidization events: three events occurred within Atlantic phylum, and four ones within Pacific group. (The karyotype of *A. brevirostrum* with 370 chromosomes was described later). Recent data on the karyotype structure of the kaluga *A. dauricus* and the Sakhalin sturgeon proving their tetraploid origins (Vasil'ev et al. 2008) assume at least three polyploidization events in Acipenserid evolution. According to these data, the only polyploidization event should be supposed for Pacific species group, whereas two polyploidization events should be presumed in Atlantic group: the origin of the common tetraploid ancestor with further speciation resulted in different tetraploid species, and the origin of hexaploid *A. brevirostrum*. However, if polyploid species originated by hybridization with triploid forms at intermediate stages, that seems most probable (Vasil'ev 1999, 2009), both triploid forms and final polyploids should possess genomes included haploid sets from different related diploid species. It means that polyploidization did not occur in different phylogenetic lineages, but resulted from the conjugation of phylogenetic lineages. In this case multiple polyploidization events should be presumed.

The study was supported by the Russian Foundation for Basic Research (grants nos. 07-04-00219, 06-04-96004-r_vostok, and 09-04-00211), by the Program "Dynamics of Gene Pools of Populations", and the Program of complex investigations in the Amur River basin FEB RAS.

Prehistory of sturgeon in the Baltic region

Stankovic A., Panagiotopoulou H., Baca M., King T.L. and Stefaniak K.

Two sturgeon species, *Acipenser oxyrinchus* and *A. sturio* are considered native for the Baltic region. According to Ludwig et al. (2002, 2008), *A. oxyrinchus* replaced *A. sturio* during the Middle Ages "little ice period". The last population of *A. sturio* still exists in the Gironde River in France while populations of *A. oxyrinchus* ceased to exist in Europe in the 20th century and survived only in the North American rivers along the Atlantic coast.

We have performed the genetic analysis of the extinct Polish population dated 2nd century BC - 13th century. The material for analyses was obtained from various archeological sites along the Vistula and Oder Rivers. We have analyzed 8 microsatellite loci and fragments of four mitochondrial genes (D-loop, 12S rDNA, 16S rDNA and cytochrome b). The same analysis was performed on five contemporary *A. oxyrinchus* populations from North America and one *A. sturio* population from the Gironde River.

The whole ancient Baltic population was monomorphic for the D-loop sequence (haplotype A). The 12S and 16S sequences were found to be identical both in Baltic and North American populations, different than in the Gironde River population. Only in the case of cytochrome b one half of the individuals forming the ancient Baltic population showed a single base substitution, typical for *A. sturio* and not found in any of the North American populations.

The population structure of all populations was deciphered basing on the microsatellite loci analysis. The genetic distance between Baltic and American (represented by the population from the St John River) populations was found to be much smaller compared to the distance between both of them and the Gironde River population. All three populations were found to pass through the bottleneck. The ancient Baltic population showed richer population structure than the remaining populations under study. It is therefore evident that already 2000 years ago the *A. oxyrinchus* population in the Baltic region was well established and was probably founded much earlier than it postulated.

Life History Strategies and Population Ecology

Salmon and Sea trout migration studies in Lithuanian rivers

Saulius Stakėnas¹, Kęstutis Skrupskelis²

¹Institute of Ecology of Vilnius University, Department of Aquatic Ecosystems, Akademijos 2, LT-2600 Vilnius, Lithuania, e-mail: saulius.stakenas@gmail.com

²Institute of Ecology of Vilnius University, Department of Aquatic Ecosystems, Akademijos 2, LT-2600 Vilnius, Lithuania, e-mail: kskrupskelis@gmail.com

Among longest freely flowing salmon and sea trout migration routes in Europe few remains in Lithuania with Žeimena River (510 km), Neris River (505 km to Belarus border) and Siesartis River (410 km to first fish ladder) maintaining numerous salmon and sea trout populations. Therefore it's very important to understand and determine